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DATE: April 30, 2013

LABORATORY REPORT

SUSPECT: Julie Fadul **NYSID NO:** 12015678R **LAB NO:** FBS13-00175
ARREST NO: B12667798 **REPORT ID:** CRT-0313-0782

RESULTS AND CONCLUSIONS:

PCR DNA typing using the AmpF*l*STR® Identifiler® PCR Amplification Kit was done on an FTA buccal swab pad from Julie Fadul. A DNA profile was determined.

The DNA profile of Julie Fadul was compared to the results in the following case:

FB Number	Complaint Number	PSNY	Case Report ID
FB13-00441	2012-050-03977	PSNY	CRT-0313-0377

Julie Fadul is excluded as the major contributor to the sample listed below. However, based on a comparison of the DNA profile of Julie Fadul to this mixture, she cannot be ruled out as a minor contributor. Two likelihood ratios were calculated for this comparison.

swab from "frontstrap, backstrap and side grips"

The DNA mixture found on the swab from "frontstrap, backstrap and side grips" is approximately **13400 times more probable** if the sample originated from Julie Fadul and one unknown, unrelated person than if it originated from two unknown, unrelated persons.

Therefore, there is very strong support that Julie Fadul and one unknown, unrelated person contributed to this mixture, rather than two unknown, unrelated persons.

The DNA mixture found on the swab from "frontstrap, backstrap and side grips" is approximately **1.06 million** times more probable if the sample originated from Julie Fadul and Kenneth Garcia than if it originated from Kenneth Garcia and one unknown, unrelated person.

Therefore, there is very strong support that Julie Fadul and Kenneth Garcia contributed to this mixture, rather than Kenneth Garcia and one unknown, unrelated person.

Julie Fadul **is excluded** as the major contributor to the sample listed below. The minor contributor was deemed not suitable for comparison.

swabs from silencer

The DNA profile above is suitable for entry into the OCME local DNA databank.

Note: This report has an associated Forensic Biology case file.

EVIDENCE RECEIVED:

ITEM	VOUCHER	DATE RECEIVED	DESCRIPTION
1.1	S057051	02/08/2013	FTA Buccal swab pad from Julie Fadul
1.2			FTA Buccal swab pad from Julie Fadul

DISPOSITION:

The following items will be retained in the laboratory:

DNA extracts from samples and controls tested

The remainder of the evidence will be returned to the OCME Evidence Unit.

Analyst : Jonathan Kui
(Criminalist, Level III)
Administrative Review Date : 04/30/2013
Administrative Reviewer : Joy Galanda

APPENDIX

Background to DNA Testing

DNA (Deoxyribo-Nucleic Acid), the inherited genetic material found in cells, contains markers which can differ from person to person. **DNA testing** can determine these genetic markers and compare biological samples from different individuals.

Alternative forms of DNA markers are called **alleles**. Alleles are found at specific areas, or locations, of the DNA called **loci** (singular, **locus**).

STR (short tandem repeat) loci contain alleles with a variable number of short repeating segments.Each STR allele can be described using a number which represents its number of repeats. A **DNA profile** is the series of numbers describing the DNA alleles found at an individual's STR DNA loci.

DNA Testing

DNA testing involves several steps, including DNA extraction, DNA quantitation, PCR/DNA amplification, and analysis of the resulting DNA alleles.

DNA extraction recovers DNA from biological samples such as blood, bone, hair, saliva, semen, and skin cells.

Differential extraction is designed to physically separate the DNA in epithelial cells from the DNA in sperm cells, in samples which potentially contain a mixture of sperm and other cell types. As a result, separate "epithelial cell," "sperm cell," and "swab (or substrate) remains" DNA fractions are generated.Incomplete separation can occur and fractions may contain both sperm DNA and epithelial cell DNA.

DNA quantitation measures the amount of DNA extracted from samples by using a technique called quantitative real time polymerase chain reaction (qRT-PCR). If sufficient DNA is detected, DNA amplification and analysis can be attempted.

The **PCR** (polymerase chain reaction) technique produces large amounts of DNA from small starting amounts of DNA by repeated cycles of copying the DNA loci (**DNA amplification**); after amplification the alleles present in the sample are identified.

PCR DNA testing for STRs uses the **Applied Biosystems AmpF*l*STR® Identifiler® PCR Amplification Kit** with 28 amplification cycles (**Identifiler® 28**) or 31 amplification cycles (**Identifiler® 31**). Each STR locus tested in the Identifiler® Kit contains between 8 and 32 identifiable alleles. The **Applied Biosystems AmpF*l*STR Minifiler™ PCR Amplification Kit may also be used**. These Kits also test the Amelogenin locus, which is used to determine the sex origin of a sample.

Y-chromosome STRs (**Y-STR**) are male-specific STRs, not present in females, that are inherited from father to son, and should be identical for all male relatives of the paternal line. For example, brothers who share the same father will have the same Y-STR type. PCR DNA testing for Y-STRs uses the **Promega Power Y kit** with 30 cycles.

Conclusions for DNA Typing

Is the source of: The DNA profile of an individual matches an evidentiary DNA profile and the population frequency of the evidentiary DNA profile meets the threshold of 1 in greater than 6.80 trillion, assuming the source is not an identical twin.

Could be the source of: The DNA profile of an individual is consistent with an evidentiary DNA profile, and the population frequency of the evidentiary DNA profile does not meet the threshold of 1 in greater than 6.80 trillion unrelated people.

Is a major or minor contributor to the mixture: The DNA profile of an individual matches a major or minor evidentiary DNA profile determined from a mixture, and the DNA population frequency of the determined major or the minor DNA profile meets the threshold of 1 in greater than 6.80 trillion individuals, assuming that source is not an identical twin.

Could be a major or minor contributor to the mixture: The DNA profile of an individual is consistent with a major or minor evidentiary DNA profile determined from a mixture, and the DNA population frequency of the determined major or the minor DNA profile does not meet the threshold of 1 in greater than 6.80 trillion unrelated people.

Could be a contributor to the mixture: For mixtures where individual profiles were not determined, all of the DNA alleles seen in an individual's DNA profile were also seen in the mixture for the locations where comparisons could be made.

Cannot be excluded as a contributor to the mixture: For the locations where comparisons could be made, most of the DNA alleles seen in an individual's DNA profile were also seen in the mixture. The allele(s) that were absent could be explained by any of several factors. Therefore, this person cannot be ruled out as a possible contributor to the mixture.

Excluded as a contributor to the mixture: For the locations where comparisons could be made, one or more of the DNA alleles seen in an individual's DNA profile were not seen in the mixture and this absence cannot be explained. Therefore, this person can be ruled out as a contributor.

No conclusions can be drawn: The results do not support a positive association or an exclusion. Therefore, it cannot be determined whether a person can or cannot be excluded to the mixture.

Not suitable for comparison: The DNA results on the evidence are either too incomplete or too complex to be the basis for conclusions regarding the source of the DNA.

Partial Match: An association between two single-source (clean or fully deconvoluted) profiles, showing similarities but short of an exact match, that suggests that the source of a profile is potentially a relative of the source of the other, partially matching, profile. Partial matches are inadvertent, and may be found at the local, state, or national levels (through comparison at the bench, LINKAGE, or CODIS searches).

Likelihood ratios:
For some mixtures wherein an individual contributor's DNA profile cannot be determined, a known person's DNA profile can still be compared to the mixture. The comparison DNA profile can be from a known person, or from a single source or deduced profile from within a case. For these comparisons, a statistical value known as a likelihood ratio (LR) may be calculated. The LR value provides a statistical measurement of the strength of support for one scenario over another, i.e., one scenario being that the known person contributed to the mixture versus the scenario that an unknown, unrelated person contributed instead.

Limited, moderate, strong or very strong support: These terms describe the strength or weakness of different ranges of a likelihood ratio (as shown in the table below). Examples of factors that affect the LR value include the amount of DNA tested, the type of mixture (for example, the number of contributors), instances when one or more of the individual's DNA alleles are not seen in the mixture, the presence of rare alleles in the mixture, and the presence of extra DNA alleles in the mixture.

Reported value	Qualitative interpretation
1	No conclusions
1 to 10	Limited support
10 to 100	Moderate support
100 to 1000	Strong support
Greater than 1000	Very strong support

Note, if the LR value is less than one, this means that the mixture is better explained if an unknown, unrelated person contributed to the mixture rather than the known person. This situation is reported as 1/LR and the qualitative terms from the table above are applied.